

SEQUENCE LISTING

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SANDROCK, ALFRED

<120> THERAPIES FOR CHRONIC INFLAMMATORY DEMYELINATING
POLYNEUROPATHY USING INTERFERON-BETA

<130> A186 US

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<160> 21

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<210> 1

<211> 840

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(639)

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gttcgtgttg tcaac atg acc aac aag tgt ctc ctc caa att gct ctc ctg 111
Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu
1 5 10

ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga 159
Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly
15 20 25

ttc cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa 207
Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln
30 35 40

ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac 255
Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp
45 50 55 60

atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc 303
Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala
65 70 75

gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga 351
Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg
80 85 90

caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc 399
Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu
95 100 105

ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa 447

Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu
 110 115 120
 gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt 495
 Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser
 125 130 135 140
 ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc 543
 Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala
 145 150 155
 aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta 591
 Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu
 160 165 170
 agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac tga 639
 Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 175 180 185
 agatctccta gcctgtgcct ctgggactgg acaattgctt caagcattct tcaaccagca 699
 gatgctgttt aagtgactga tggctaattgt actgcatatg aaaggacact agaagatttt 759
 gaaattttta ttaaattatg agttattttt atttatttaa attttatttt ggaaaataaa 819
 ttatttttgg tgcaaaagtc a 840

<210> 2
 <211> 187
 <212> PRT
 <213> Homo sapiens

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 Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
 20 25 30
 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
 35 40 45
 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60
 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80
 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95
 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125
 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145 150 155 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
180 185

<210> 3
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(501)

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Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
1 5 10 15
tgt cag aag ctc ctg tgg caa ttg aat ggg agg ctt gaa tac tgc ctc 96
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
20 25 30
aag gac agg atg aac ttt gac atc cct gag gag att aag cag ctg cag 144
Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
35 40 45
cag ttc cag aag gag gag gac gcc gca ttg acc atc tat gag atg ctc cag 192
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
50 55 60
aac atc ttt gct att ttc aga caa gat tca tct agc act ggc tgg aat 240
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
65 70 75 80
gag act att gtt gag aac ctc ctg gct aat gtc tat cat cag ata aac 288
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
85 90 95
cat ctg aag aca gtc ctg gaa gaa aaa ctg gag aaa gaa gat ttc acc 336
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
100 105 110
agg gga aaa ctc atg agc agt ctg cac ctg aaa aga tat tat ggg agg 384
Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
115 120 125
att ctg cat tac ctg aag gcc aag gag tac agt cac tgt gcc tgg acc 432
Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
130 135 140
ata gtc aga gtg gaa atc cta agg aac ttt tac ttc att aac aga ctt 480
Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
145 150 155 160
aca ggt tac ctc cga aac tga 501

Thr Gly Tyr Leu Arg Asn
165

<210> 4
<211> 166
<212> PRT
<213> Homo sapiens

<400> 4
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Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
20 25 30
Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
35 40 45
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
50 55 60
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
65 70 75 80
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
85 90 95
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
100 105 110
Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
115 120 125
Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
130 135 140
Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
145 150 155 160
Thr Gly Tyr Leu Arg Asn
165

<210> 5
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
illustrative oligonucleotide

<400> 5
ggcgggtggtg gcagc

15

<210> 6
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 6
Gly Gly Gly Gly Ser
1 5

<210> 7
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
illustrative oligonucleotide

<400> 7
gacgatgatg acaag

15

<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
enterokinase recognition site

<400> 8
Asp Asp Asp Asp Lys
1 5

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
illustrative oligonucleotide

<400> 9
agctccggag acgatgatga caag

24

<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 10
Ser Ser Gly Asp Asp Asp Asp Lys

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5

<210> 11

<211> 1257

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct sequence

<220>

<221> CDS

<222> (1)..(1254)

<400> 11

atg cct ggg aag atg gtc gtg atc ctt gga gcc tca aat ata ctt tgg	48
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1 5 10 15	
ata atg ttt gca gct tct caa gcc atg agc tac aac ttg ctt gga ttc	96
Ile Met Phe Ala Ala Ser Gln Ala Met Ser Tyr Asn Leu Leu Gly Phe	
20 25 30	
cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa ttg	144
Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu	
35 40 45	
aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac atc	192
Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile	
50 55 60	
cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc gca	240
Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala	
65 70 75 80	
ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga caa	288
Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln	
85 90 95	
gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc ctg	336
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu	
100 105 110	
gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa gaa	384
Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu	
115 120 125	
aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt ctg	432
Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu	
130 135 140	
cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc aag	480
His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys	
145 150 155 160	
gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta agg	528
Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg	
165 170 175	

aac ttt tac ttc att aac aga ctt aca tgt tac ctc cga aac gtc gac	576
Asn Phe Tyr Phe Ile Asn Arg Leu Thr Cys Tyr Leu Arg Asn Val Asp	
180 185 190	
aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga	624
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly	
195 200 205	
ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc	672
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile	
210 215 220	
tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa	720
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu	
225 230 235 240	
gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat	768
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His	
245 250 255	
aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt	816
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg	
260 265 270	
gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag	864
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys	
275 280 285	
gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag	912
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu	
290 295 300	
aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac	960
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr	
305 310 315 320	
acc ctg ccc cca tcc ccg gat gag ctg acc aag aac cag gtc agc ctg	1008
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu	
325 330 335	
acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg	1056
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp	
340 345 350	
gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg	1104
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val	
355 360 365	
ttg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac	1152
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp	
370 375 380	
aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat	1200
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His	
385 390 395 400	
gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccc	1248
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro	
405 410 415	
ggg aaa tga	1257

Gly Lys

<210> 12

<211> 418

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
fusion protein sequence

<400> 12

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Ile Met Phe Ala Ala Ser Gln Ala Met Ser Tyr Asn Leu Leu Gly Phe
20 25 30

Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu
35 40 45

Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile
50 55 60

Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala
65 70 75 80

Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
85 90 95

Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu
100 105 110

Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu
115 120 125

Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu
130 135 140

His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys
145 150 155 160

Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg
165 170 175

Asn Phe Tyr Phe Ile Asn Arg Leu Thr Cys Tyr Leu Arg Asn Val Asp
180 185 190

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
195 200 205

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
210 215 220

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
225 230 235 240

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
245 250 255

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 260 265 270
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 275 280 285
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 290 295 300
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 305 310 315 320
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 325 330 335
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 340 345 350
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 355 360 365
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 370 375 380
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 385 390 395 400
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 405 410 415

Gly Lys

<210> 13

<211> 1272

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct sequence

<220>

<221> CDS

<222> (1)..(1269)

<400> 13

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Met	Pro	Gly	Lys	Met	Val	Val	Ile	Leu	Gly	Ala	Ser	Asn	Ile	Leu	Trp	
1				5					10					15		

ata	atg	ttt	gca	gct	tct	caa	gcc	atg	agc	tac	aac	ttg	ctt	gga	ttc	96
Ile	Met	Phe	Ala	Ala	Ser	Gln	Ala	Met	Ser	Tyr	Asn	Leu	Leu	Gly	Phe	
			20					25					30			

cta	caa	aga	agc	agc	aat	ttt	cag	tgt	cag	aag	ctc	ctg	tgg	caa	ttg	144
Leu	Gln	Arg	Ser	Ser	Asn	Phe	Gln	Cys	Gln	Lys	Leu	Leu	Trp	Gln	Leu	
		35				40						45				

aat	ggg	agg	ctt	gaa	tac	tgc	ctc	aag	gac	agg	atg	aac	ttt	gac	atc	192
Asn	Gly	Arg	Leu	Glu	Tyr	Cys	Leu	Lys	Asp	Arg	Met	Asn	Phe	Asp	Ile	

50	55	60	
cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc gca Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala 65 70 75 80			240
ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga caa Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln 85 90 95			288
gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc ctg Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu 100 105 110			336
gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa gaa Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu 115 120 125			384
aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt ctg Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu 130 135 140			432
cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc aag His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys 145 150 155 160			480
gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta agg Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg 165 170 175			528
aac ttt tac ttc att aac aga ctt aca tgt tac ctc cga aac ggc ggt Asn Phe Tyr Phe Ile Asn Arg Leu Thr Cys Tyr Leu Arg Asn Gly Gly 180 185 190			576
ggt ggc agc gtc gac aaa act cac aca tgc cca ccg tgc cca gca cct Gly Gly Ser Val Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro 195 200 205			624
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys 210 215 220			672
gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val 225 230 235 240			720
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp 245 250 255			768
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 260 265 270			816
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp 275 280 285			864
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu 290 295 300			912

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	960
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
305 310 315 320	
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag	1008
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	
325 330 335	
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	1056
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
340 345 350	
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag	1104
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys	
355 360 365	
acc acg cct ccc gtg ttg gac tcc gac ggc tcc ttc ttc ctc tac agc	1152
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser	
370 375 380	
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca	1200
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser	
385 390 395 400	
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc	1248
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser	
405 410 415	
ctc tcc ctg tct ccc ggg aaa tga	1272
Leu Ser Leu Ser Pro Gly Lys	
420	

<210> 14
 <211> 423
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 fusion protein sequence

<400> 14

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Ile	Met	Phe	Ala	Ala	Ser	Gln	Ala	Met	Ser	Tyr	Asn	Leu	Leu	Gly	Phe
			20					25					30		
Leu	Gln	Arg	Ser	Ser	Asn	Phe	Gln	Cys	Gln	Lys	Leu	Leu	Trp	Gln	Leu
		35					40					45			
Asn	Gly	Arg	Leu	Glu	Tyr	Cys	Leu	Lys	Asp	Arg	Met	Asn	Phe	Asp	Ile
	50					55					60				
Pro	Glu	Glu	Ile	Lys	Gln	Leu	Gln	Gln	Phe	Gln	Lys	Glu	Asp	Ala	Ala
65					70					75					80
Leu	Thr	Ile	Tyr	Glu	Met	Leu	Gln	Asn	Ile	Phe	Ala	Ile	Phe	Arg	Gln
				85					90					95	

Asp	Ser	Ser	Ser	Thr	Gly	Trp	Asn	Glu	Thr	Ile	Val	Glu	Asn	Leu	Leu		
			100					105					110				
Ala	Asn	Val	Tyr	His	Gln	Ile	Asn	His	Leu	Lys	Thr	Val	Leu	Glu	Glu		
		115					120					125					
Lys	Leu	Glu	Lys	Glu	Asp	Phe	Thr	Arg	Gly	Lys	Leu	Met	Ser	Ser	Leu		
	130					135					140						
His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg	Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys		
145					150					155					160		
Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr	Ile	Val	Arg	Val	Glu	Ile	Leu	Arg		
				165					170						175		
Asn	Phe	Tyr	Phe	Ile	Asn	Arg	Leu	Thr	Cys	Tyr	Leu	Arg	Asn	Gly	Gly		
			180					185					190				
Gly	Gly	Ser	Val	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro		
		195					200					205					
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys		
	210					215					220						
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val		
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Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp		
				245					250					255			
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr		
			260					265					270				
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp		
		275					280					285					
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu		
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Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg		
305					310					315					320		
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys		
				325					330					335			
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp		
			340					345					350				
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys		
		355					360					365					
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser		
	370					375					380						
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser		
385					390					395					400		
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser		
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